

| Sequences producing significant alignments: | Score (bits) | E Value |
|---|-----------------|------------|
| gi 5771354 dbj BAA83501.1 Sucrose Transporter [Zea mays] | 449 | e-124 |
| gi 9624451 gb AAF90181.1 sucrose transporter [Oryza sativa...] | 356 | 1e-96 |
| gi 7489560 pir T02982 probable sucrose transport protein -... | 353 | 9e-96 |
| gi 7024415 emb CAB75882.1 sucrose transporter 1 [Hordeum v... | 330 | 7e-89 |
| gi 20152871 gb AAM13408.1 sucrose transporter SUT1A [Triti... | 303 | 8e-81 |
| gi 19548165 gb AAL90455.1 sucrose transporter SUT1D [Triti... | 301 | 5e-80 |
| gi 20152873 gb AAM13409.1 sucrose transporter SUT1B [Triti... | 297 | 5e-79 |
| gi 15718401 dbj BAB68368.1 sucrose transporter [Oryza sati... | 252 | 3e-65 |
| gi 19071641 gb AAL84308.1 sucrose transporter, 5'-partial ... | 238 | 4e-61 |
| gi 16152148 gb AAL14982.1 sucrose transporter [Oryza sativ... | 187 | 1e-45 |
| gi 15217323 gb AAK92667.1 Putative sucrose transporter [Or... | 157 | 1e-36 |
| gi 37534172 ref NP_921388.1 putative sucrose transporter [...] | 156 | 2e-36 |
| gi 29467456 dbj BAC67165.1 sucrose transporter [Oryza sati... | 137 | 9e-31 |
| gi 37548736 gb AAN15219.1 sucrose transporter SUT2 [Oryza ...] | 89 | 4e-16 |
| gi 10119908 gb AAG12987.1 sucrose transporter-like protein... | 88 | 6e-16 |
| gi 31096339 gb AAP43631.1 sucrose transporter-like protein... | 88 | 1e-15 |
| gi 29467454 dbj BAC67164.1 sucrose transporter [Oryza sati... | 85 | 5e-15 |

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|-------------------------------|--|----|-------|
| gi 6434831 gb AAF08330.1 | putative sucrose transporter [Vit... | 85 | 5e-15 |
| gi 21063927 gb AAM29153.1 | sucrose transporter 2 [Citrus si... | 84 | 1e-14 |
| gi 31455370 emb CAD58887.1 | sucrose transporter [Plantago m... | 80 | 2e-13 |
| gi 15227049 ref NP_178389.1 | sucrose transporter / sucrose... | 75 | 7e-12 |
| gi 42570661 ref NP_973404.1 | sucrose transporter / sucrose... | 75 | 7e-12 |
| gi 14161682 gb AAK54857.1 | sucrose transporter [Oryza sativa] | 74 | 1e-11 |
| gi 14161680 gb AAK54856.1 | sucrose transporter [Oryza sativa] | 74 | 1e-11 |
| gi 7488935 pir T14339 | sucrose-proton transport protein - c... | 70 | 2e-10 |
| gi 17447420 gb AAF04295.2 | sucrose transporter 1 [Alonsoa m... | 70 | 2e-10 |
| gi 29467452 dbj BAC67163.1 | sucrose transporter [Oryza sati... | 66 | 3e-09 |
| gi 1076644 pir IS48789 | sucrose transport protein - common t... | 66 | 3e-09 |
| gi 15219686 ref NP_176830.1 | sucrose transporter, putative ... | 64 | 1e-08 |
| gi 549000 sp Q03411 SUT SPIOL | Sucrose transport protein (Su... | 63 | 4e-08 |
| gi 38327323 gb AAR17700.1 | sucrose transporter [Malus x dom... | 62 | 6e-08 |
| gi 15239921 ref NP_199174.1 | sucrose transporter-related / ... | 62 | 6e-08 |
| gi 20147213 gb AAM10322.1 | At1g22710/T22J18_12 [Arabidopsis... | 58 | 7e-07 |
| gi 15219938 ref NP_173685.1 | sucrose transporter / sucrose... | 58 | 7e-07 |
| gi 481131 pir S38196 | sucrose transport protein SUC2 - Arab... | 58 | 9e-07 |
| gi 10998390 gb AAG25923.1 | sucrose transporter SUT4 [Solanu... | 57 | 2e-06 |
| gi 9957218 gb AAG09270.1 | sucrose transporter [Lycopersicon... | 57 | 2e-06 |
| gi 15225986 ref NP_179074.1 | sucrose transporter, putative ... | 56 | 3e-06 |
| gi 30349815 emb CAD31122.1 | putative sucrose-H ⁺ symporter [... | 56 | 4e-06 |
| gi 18091781 gb AAL58072.1 | sucrose transporter SUC2 [Brassi... | 55 | 7e-06 |
| gi 9957053 gb AAG09191.1 | sucrose transporter SUT4 [Arabido... | 55 | 1e-05 |
| gi 25344709 pir A86234 | hypothetical protein [imported] - A... | 55 | 1e-05 |
| gi 15218362 ref NP_172467.1 | sucrose transporter / sucrose... | 55 | 1e-05 |
| gi 5823000 gb AAD53000.1 | sucrose-proton symporter [Beta vu... | 54 | 2e-05 |
| gi 1076257 pir S51114 | sucrose-proton symporter - beet >gi ... | 54 | 2e-05 |
| gi 7649151 gb AAF65765.1 | sucrose transport protein [Euphor... | 53 | 2e-05 |
| gi 28172870 emb CAD61275.1 | sucrose transporter 4 protein [... | 53 | 2e-05 |
| gi 15239949 ref NP_196235.1 | sucrose transporter, putative ... | 53 | 3e-05 |
| gi 542087 pir JQ2389 | sucrose transport protein - potato >g... | 53 | 3e-05 |
| gi 575299 emb CAA57726.1 | sucrose transporter [Lycopersicon... | 52 | 4e-05 |
| gi 1076602 pir S48788 | sucrose transport protein - tomato (... | 52 | 4e-05 |
| gi 27447671 gb AAO13696.1 | sucrose transporter [Lycopersico... | 52 | 4e-05 |
| gi 6120115 gb AAF04294.1 | sucrose transporter 1 [Asarina ba... | 52 | 6e-05 |
| gi 4091891 gb AAC99332.1 | sucrose transporter [Apium graveo... | 52 | 6e-05 |
| gi 5230818 gb AAD41024.1 | sucrose transport protein SUT1 [P... | 52 | 6e-05 |
| gi 7024413 emb CAB75881.1 | sucrose transporter 2 [Hordeum v... | 52 | 6e-05 |
| gi 5566434 gb AAD45390.1 | sucrose transporter SUT2A [Apium ... | 52 | 6e-05 |
| gi 33620334 emb CAD91334.1 | sucrose transporter [Glycine max] | 52 | 6e-05 |
| gi 7488866 pir T12198 | sucrose transport protein - fava bea... | 52 | 6e-05 |
| gi 27227722 emb CAD29832.1 | sucrose transporter [Viscum alb... | 52 | 7e-05 |
| gi 12038843 emb CAC19689.1 | sucrose/proton symporter [Daucu... | 52 | 7e-05 |
| gi 7488936 pir T14340 | sucrose-proton transport protein - c... | 52 | 7e-05 |
| gi 16930709 gb AAL32020.1 | sucrose transporter [Vitis vinif... | 52 | 7e-05 |
| gi 6705993 dbj BAA89458.1 | sucrose transporter protein [Dau... | 52 | 7e-05 |
| gi 1086250 pir S52377 | sucrose transport protein SUC1 - com... | 51 | 1e-04 |
| gi 6434833 gb AAF08331.1 | putative sucrose transporter [Vit... | 51 | 1e-04 |
| gi 542020 pir S43142 | sucrose transport protein - castor be... | 51 | 1e-04 |
| gi 5640023 gb AAD45932.1 | sucrose transport protein [Betula... | 51 | 1e-04 |
| gi 13186184 emb CAC33492.1 | sucrose carrier [Ricinus communis] | 50 | 2e-04 |
| gi 1086253 pir S38657 | sucrose transport protein ptpl - com... | 50 | 2e-04 |
| gi 18091779 gb AAL58071.1 | sucrose transporter SUC1 [Brassi... | 50 | 2e-04 |
| gi 12057172 emb CAC19851.1 | sucrose trasporter [Arabidopsis... | 50 | 2e-04 |
| gi 15217602 ref NP_177334.1 | sucrose transporter / sucrose... | 50 | 2e-04 |
| gi 28143940 gb AAO26335.1 | putative sucrose transporter [Br... | 50 | 2e-04 |
| gi 5882292 gb AAD55269.1 | sucrose transporter [Vitis vinifera] | 49 | 6e-04 |
| gi 35187437 gb AAQ84310.1 | fiber sucrose transporter [Gossy... | 49 | 6e-04 |
| gi 2980887 emb CAA12256.1 | Sucrose carrier [Ricinus communis] | 48 | 8e-04 |

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|-------------------------------|--|----|-------|
| gi 21063921 gb AAM29150.1 | citrus sucrose transporter 1 [Citrus... | 48 | 0.001 |
| gi 15217601 ref NP_177333.1 | sucrose transporter / sucrose-... | 47 | 0.001 |
| gi 28371870 gb AAO38059.1 | sucrose transporter SUC1 [Brassica... | 46 | 0.003 |
| gi 4960089 gb AAD34610.1 | sucrose transporter-like protein ... | 45 | 0.008 |
| gi 6434829 gb AAF08329.1 | putative sucrose transporter [Vitis... | 44 | 0.011 |
| gi 12322260 gb AAG51155.1 | sucrose-proton symporter, 5' par... | 43 | 0.027 |
| gi 4586604 dbj BAA76434.1 | sucrose transport protein [Cicer... | 39 | 0.51 |
| gi 26522780 dbj BAC44864.1 | hypothetical protein [Glycine max] | 38 | 0.68 |
| gi 40287430 gb AAR83844.1 | glycogen debranching enzyme [Bren... | 38 | 1.2 |
| gi 30349806 emb CAD30831.1 | putative sucrose-H ⁺ symporter [... | 36 | 4.0 |
| gi 22298694 ref NP_681941.1 | permease protein of oligopeptid... | 36 | 4.0 |
| gi 40788373 dbj BAA74844.2 | KIAA0821 protein [Homo sapiens] | 35 | 7.1 |
| gi 7513937 pir T17138 | CL1AA protein - rat >gi 2213659 gb A... | 35 | 7.1 |
| gi 38089363 ref XP_134383.4 | latrophilin 1 [Mus musculus] | 35 | 7.1 |
| gi 41281557 ref NP_055736.2 | latrophilin 1; lectomedin-2 [Homo... | 35 | 7.1 |
| gi 28972417 dbj BAC65662.1 | mKIAA0821 protein [Mus musculus] | 35 | 7.1 |
| gi 22969021 ref ZP_00016596.1 | COG0477: Permeases of the major... | 35 | 7.1 |
| gi 7513940 pir T17156 | CL1BB protein - rat >gi 3695121 gb A... | 35 | 7.1 |
| gi 21929099 dbj BAC06134.1 | seven transmembrane helix receptor | 35 | 7.1 |
| gi 12621148 ref NP_075251.1 | CL1BA protein [Rattus norvegicus] | 35 | 7.1 |
| gi 7513938 pir T17145 | CL1AB protein - rat >gi 3695117 gb A... | 35 | 7.1 |
| gi 23110155 ref ZP_00096317.1 | COG1448: Aspartate/tyrosine/... | 35 | 7.1 |
| gi 14043198 gb AAH07587.1 | LPHN1 protein [Homo sapiens] | 35 | 7.1 |

Alignments

>gi|5771354|dbj|BAA83501.1| Sucrose Transporter [Zea mays]
Length = 521

Score = 449 bits (1052), Expect = e-124
Identities = 255/684 (37%), Positives = 271/684 (39%), Gaps = 399/684 (58%)

Query: 42 GQLAELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQT 78
G+L ELS GV DHVAPISLG MVAGGVQYGW LTPYVQT

Sbjct: 6 GEL-ELSVGVRGTGGAAAAAAADHVAPISLGLRLILAGMVAGGVQYGWALQLSLLTPYVQT 64

Query: 79 LGLG-PIAGDRCTSFMWLC-----VGLYS-----PFILTGCMLIIGAA 115
LGL + TSFMWLC VGLYS PFIL GCMLI

Sbjct: 65 LGLSHAL----TSFMWLCGPIAGLVVQPLVGLYSDRCTARWGRRRPFILIGCMLI---- 115

Query: 116 HGPRWLLDFSMADLCFCSSSTNNWWETCCEAVFLVLVPYRAEVETECVAVIV----- 166
C+AVIV

Sbjct: 116 -----CLAVIVVGFSIDGA 130

Query: 167 ---DTKE---L--G---HAAIVY-----NNTVQG-----D---HHGPSA--- 191
DTKE L G HAAIVY NNTVQG D HHGPSA

Sbjct: 131 ALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSNNTVQGPARAMMADLCGHGHPAANSI 190

Query: 192 -----LGNIL-----KWFVFVGFSDDHCSLYVLGFWPARAMA-ANSIGYSSGL 233
LGNIL KWFVF+ ++ C A AN L

Sbjct: 191 FCSWMALGNILGYSSGSTNNWHKWFPL-LTNACCE-----ACAN-----L 230

Query: 234 KTS AFLV AVI FAK EAN LKG A CLTV TL ----- NEN LPTT KAG G ----- PTGPL A LA 278
 K AFLV AV+ F L CLTV TL N+NLP TKA G P+GP LA
 Sbjct: 231 K-G AFLV AVVF ----- L-VM CLTV TL FF FANE VPY RGN QNLP -TK ANGE VETE PSGP -- LA 280

Query: 279 VLK ----- MPSV LL VT ----- FP FILY DTD HGD PKL Y SAG FKDL PPA ITW L SW W 323
 VLK MPSV LL VT FP FILY DTD W
 Sbjct: 281 VLK GFK NL PTG MPSV LL VT GLT WLSW FP FILY DTD ----- W 316

Query: 324 MG REI Y ----- QIS AFNE ----- LLL NSV IL ----- PM CRK VGP ----- 352
 MG REI Y QIS AFNE LLL NSV IL PM CRK VGP
 Sbjct: 317 MG REI Y HG DPK GSNA QIS AF DEG V RVG SFG LLL NSIV LG FSS FLIE PM CRK VGP RVV W VT 376

Query: 353 -- FMV C V A MA ----- SL RDY HGY ----- SIK A VC S V R V G A F G G F S S F L I E R 393
 FMV C V A MA SL+DY HGY SIK A VC V L
 Sbjct: 377 SNF M V C V A M A A T A L I S F W S L K D Y H G Y V Q D A I T A S T S I K A V C L V ----- L --- 420

Query: 394 V V W V T S N I S F W I T A N A F L G V P T A Q L A A T A L V Q D A V L F A - P F A V ----- GL C T G 440
 F AFL G V P L A+L++ P F A V GL C T G
 Sbjct: 421 ----- F ----- AFL G V P -- L ----- A I L Y S V P F A V T A Q L A A T K G G G Q G L C T G 455

Query: 441 V L N I A T R G G G Q S I V I P Q V I I A L ----- N I P A F ----- V V G V F A V S A G 477
 V L N I S I V I P Q V I I A L N I P A F V V G V F
 Sbjct: 456 V L N I ----- S I V I P Q V I I A L G A G P W D A L F G K G N I P A F G V A S G F A L I G G V V G F ----- 503

Query: 478 G G V A S A L L P K I G H F A L V G S K R Q F R 501
 L L P K I S K R Q F R
 Sbjct: 504 ----- L L P K I ----- S K R Q F R 514

Score = 71.0 bits (160), Expect = 1e-10
 Identities = 41/105 (39%), Positives = 41/105 (39%), Gaps = 64/105 (60%)

Query: 1 M A R G D G ----- R G ----- A A A -- V ----- R L I L A G ----- A L Q L S L ----- 24
 M A R G D G R G A A A V R L I L A G A L Q L S L
 Sbjct: 1 M A R G D G E L E L S V G V R G T G G A A A A A D H V A P I S L G R L I L A G M V A G G V Q Y G W A L Q L S L L T P 60

Query: 25 ----- S H A L T S ----- V V Q P L ----- R W G R R R 41
 S H A L T S V V Q P L R W G R R R
 Sbjct: 61 Y V Q T L G L S H A L T S F M W L C G P I A G L V V Q P L V G L Y S D R C T A R W G R R R 105

>gi|9624451|gb|AAF90181.1| sucrose transporter [Oryza sativa (indica cultivar-gr
 Length = 538

Score = 356 bits (833), Expect = 1e-96
 Identities = 231/695 (33%), Positives = 254/695 (36%), Gaps = 422/695 (60%)

Query: 46 E L S A G V ----- V D H V A P I S L G ----- M V A G G V Q Y G W ----- L T P Y V 76
 E L S G V V + A P I S L G M V A G G V Q Y G W L T P Y V
 Sbjct: 19 E L S V G V G G G G A R G G G G E A A A V E T A A P I S L G R L I L S G M V A G G V Q Y G W A L Q L S L L T P Y V 78

Query: 77 Q T L G L G - P I A G D R C T S F M W L C ----- V G L Y S ----- P F I L T G C M L I I G 113
 Q T L G L + T S F M W L C V G L Y S P + I L T G C + L I
 Sbjct: 79 Q T L G L S H A L ----- T S F M W L C G P I A G M V V Q P C V G L Y S D R C T S K W G R R R P Y I L T G C V L I -- 131

Query: 114 A A H G P R W L L D F S M A D L C F C S S T N N W E T C C E A V F L V L V P Y R A E V E T E C V A V I V ----- 166
 C + A V + V

Sbjct: 132 -----CLAVVIVGFSADI 144
 Query: 167 ----DTKE----LG---HAAIVYNNNTVQGDHHGPSALGNILKWFPFVGFFSSDHCSLYV 213
 DTKE G HAAIVY V
 Sbjct: 145 GYAMGDTKEDCSVYHGSRWHAIVY-----V 170
 Query: 214 LGFW-----PARA-MA-----ANSI-----GYSSG----- 232
 LGFW PARA MA ANSI GYSSG
 Sbjct: 171 LGFWLDFSNNTVQGPARALMADLSGRHGPCTANSIFCSWMAMGNILGYSSGSTNNWHKW 230
 Query: 233 ---LKT-----SAFLVAVIFAKEANLKGACLTVTL-----NENLPTTKA 268
 LKT AFLVAVIF +L CL +TL N LPT K+
 Sbjct: 231 FPFLKTRACCEACANLKGAFLVAVIFL---SL---CLVITLIFAKEVPFKGNAALPT-KS 283
 Query: 269 GGP-----TGPLALAVLK-----MPSVLLVTFPFILYDTDHGDPKLYSNAGFKDLPP 315
 P TGPLA VLK MPSVL+VT
 Sbjct: 284 NEPAEPEGTGPLA--VLKGFRNLPTGMPSVLIVT----- 315
 Query: 316 AITWLSW-----WMGREIY-----QISAFNE-----LLLNSVIL---- 344
 +TWLSW WMGREIY QI AFN+ LLLNS++L
 Sbjct: 316 GLTWLSWFPFILYDTDWMGREIYHGDPKGTDQIEAFNQGVRAGAFGLLNSIVLGFFF 375
 Query: 345 ---PMCRKVGP-----FMVCVAMA-----SLRDYHGY-----SIKAVCSV 376
 PMCRKVGP F+VC+AMA SL+D+HG SIKAVC V
 Sbjct: 376 LIEPMCRKVGPVVWVTSNFLCIAAMAATALISFWSLKDHFHGTQKAITADKSIKAVCLV 435
 Query: 377 GVRVGAFFGFSFLIERVVWVTSNISFWITANAFLGVPTAQLAATALVQDAVLFA-PFAV 435
 L F AFLGV P L AVL++ PFAV
 Sbjct: 436 -----L-----F-----AFLGV P-----AVLYSVPFAV 454
 Query: 436 -----GLCTGVLNIASTRGGGQSIVIPQVIIAL-----NIPAFVVGV 471
 GLCTGVLN SIVIPQV+IAL NIPAF G+
 Sbjct: 455 TAQLAATRGGGQGLCTGVLN SIVIPQVIALGAGPWDELFGKGNIPAF--GL 505
 Query: 472 ---FA-VSAGGGVASA-LLPKIGHFALVGSKRQFR 501
 FA + GGVA LLPKI SKRQFR
 Sbjct: 506 ASGFALI---GGVAGIFLLPKI-----SKRQFR 530

Score = 84.6 bits (192), Expect = 8e-15
 Identities = 78/285 (27%), Positives = 83/285 (29%), Gaps = 195/285 (68%)

Query: 2 ARGDGRG--AAAV-----RLILAG-----ALQLSL-----SHALTS 30
 ARG G G AAAV RLIL+G ALQLSL SHALTS
 Sbjct: 30 ARGGGGGEAAA VETAAPISLGLRLLSGMVAGGVQYQWALQLSLLTPYVQTLGLSHALTS 89
 Query: 31 -----VVQP---L-----RWGRRRGQLAELSAGVVDHVAPISLGMVAGGVQY 69
 VVQP L +WGR
 Sbjct: 90 FMWLCGPIAGMVVQPCVGLYSDRCTSKWGR----- 121
 Query: 70 GWLTPYVQTLGLGPIAGDRCTSFMWLCVGLYSPFILTGCMLI-----IGAA-- 115
 PY+ LTGC+LI IG A
 Sbjct: 122 -----PYI-----LTGCVLICLAVVIVGFSADIGYAMG 149
 Query: 116 -----HGPR-----WLLDFS-----MADLC-----FCS 133
 HG R WLLDFS MADL FCS
 Sbjct: 150 DTKEDCSVYHGSRWHAIVYVLGFWLLDFSNNTVQGPARALMADLSGRHGPCTANSIFCS 209
 Query: 134 -----STNNW--W----ET--CCEA-----VFLVLV 151

STNNW W +T CCEA FLV V
 Sbjct: 210 WMAMGNILGYSSGSTNNWHKFPLKTRACCEACANLKGAFLVAV 254

[>gi|7489560|pir||T02982] probable sucrose transport protein - rice
 gi|2723471|dbj|BAA24071.1| sucrose transporter [Oryza sativa (japonica cultivar-g
 Length = 537

Score = 353 bits (826), Expect = 9e-96
 Identities = 230/693 (33%), Positives = 253/693 (36%), Gaps = 421/693 (60%)

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQ 77
 ELS GV V+ APISLG MVAGGVQYGW LTPYVQ
 Sbjct: 19 ELSVGVGGGARGGGGEAAA VETAAPISLGLRILSGMVAGGVQYGWALQLSLLTPYVQ 78

Query: 78 TLGLG-PIAGDRCTSFMWLC-----VGLYS-----PFILTGCMLIIGA 114
 TLGL + TSFMWLC VGLYS P+ILTGC+LI
 Sbjct: 79 TLGLSHAL-----TSFMWLCGPIAGMVVQPCVGLYSRDRCTSKWGRRRPYILTGCVLI--- 130

Query: 115 AHGPRWLDFSMADLCFCSSSTNNWETCCEAVFLVLVPYRAEVETECVAVIV----- 166
 C+AV+V
 Sbjct: 131 -----CLAVVVIGFSADIG 144

Query: 167 ----DTKE----LG---HAAIVVNNTVQGDHHGPSALGNILKWFVGFSSDHCSLYVL 214
 DTKE G HAAIVY VL
 Sbjct: 145 YAMGDTKEDCSVYHGSRWHAIIIVY-----VL 170

Query: 215 GFW-----PARA-MA-----ANSI-----GYSSG----- 232
 GFW PARA MA ANSI GYSSG
 Sbjct: 171 GFWLDFSNNTVQGPARALMADLSGRHGP GTANSIFCSWMAMGNILGYSSGSTNNWHKF 230

Query: 233 --LKT-----SAFLVAVIFAKEANLKGACLT VTL-----NENLPTTKAG 269
 LKT AFLVAVIF +L CL +TL N LPT K+
 Sbjct: 231 PFLKTRACCEACANLKGAFLVAVIFL---SL---CLVITLIFAKEVVPFKGNAALPT-KSN 283

Query: 270 GP-----TGPLALAVLK-----MPSVLLVTFPFILYDTDHGDPKLYSNAGFKDLPPA 316
 P TGPLA VLK MPSVLT+VT
 Sbjct: 284 EPAEPEGTGPLA--VLKGFRNLPTGMPSVLIVT-----G 315

Query: 317 ITWLSW-----WMGREIY-----QISAFNE-----LLLNSVIL----- 344
 +TWLSW WMGREIY QI AFN+ LLLNS++L
 Sbjct: 316 LTWLSWFPFILYDTDWMGREIYHGDPKGTDQTEAFNQGVVRAGAFGLLNSIVLGFSSFL 375

Query: 345 --PMCRKVGP-----FMVCVAMA-----SLRDYHGY-----SIKAVCSVG 377
 PMCRKVGP F+VC+AMA SL+D+HG SIKAVC V
 Sbjct: 376 IEPMCRKVGPVWWVTSNFLVCIAMAATALISFWSLKDFHGTQKAITADKSIKAVCLV- 434

Query: 378 VRVGAFFGFSFLIERVVWVTSNISFWITANAFLGVPTAQLAATALVQDAVLFA-PFAV- 435
 L F AFLGV P L AVL++ PFAV
 Sbjct: 435 -----L-----F-----AFLGV P-----L-----AVLYSVPFAVT 454

Query: 436 -----GLCTGVLNIA TRGGGQSIVIPQVIIAL-----NI PAFVVGV- 471
 GLCTGVLNIA SIVIPQV+IAL NI PAF G+
 Sbjct: 455 AQLAATRGQQGLCTGVLNIA-----SIVIPQVIA LGAGPWDELFKGKNI PAF--GLA 505

Query: 472 --FA-VSAGGGVASA-LLPKIGHFALVGSKRQF 500
 FA + GGVA LLPKI SKRQF
 Sbjct: 506 SGFALI---GGVAGIFLLPKI-----SKRQF 528

Score = 84.6 bits (192), Expect = 8e-15
 Identities = 78/285 (27%), Positives = 83/285 (29%), Gaps = 195/285 (68%)

Query: 2 ARGDGRG--AAAV-----RLILAG-----ALQLSL-----SHALTS 30
 ARG G G AAAV RLIL+G ALQLSL SHALTS
 Sbjct: 29 ARGGGGGEAAAATAAPISLGRLLISGMVAGGVQYGVWALQLSLLTPVQTLGLSHALTS 88

Query: 31 -----VVQP---L-----RWGRRRGQLAELSAGVVDHVAPISLGMVAGGVQY 69
 VVQP L +WGRRL
 Sbjct: 89 FMWLCGPIAGMVVQPCVGLYSDRCTSKWGRRL----- 120

Query: 70 GWLTPYVQTLGLGPIAGDRCTSFWMWCGLYSPFILTGCMLI-----IGAA-- 115
 PY+ LTGC+LI IG A
 Sbjct: 121 ----PYI-----LTGCVLICLAVVIGFSADIGYAMG 148

Query: 116 -----HGPR-----WLLDFS-----MADLC-----FCS 133
 HG R WLLDFS MADL FCS
 Sbjct: 149 DTKEDCSVYHGSRWHAIVYVLGFWLDFSNNTVQGPARALMADLSGRHGPCTANSIFCS 208

Query: 134 -----STNNW--W---ET--CCEA----VFLVLV 151
 STNNW W +T CCEA FLV V
 Sbjct: 209 WMAMGNILGYSSGSTNNWHKFPLKTRACCEACANLKGAFLVAV 253

□>gi|7024415|emb|CAB75882.1| sucrose transporter 1 [Hordeum vulgare subsp. vulgar
 Length = 523

Score = 330 bits (772), Expect = 7e-89
 Identities = 223/685 (32%), Positives = 253/685 (36%), Gaps = 408/685 (59%)

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGV-----LTPYVQTLGLG 82
 ELS GV + ISLG MVAGGVQYGV LTPYVQTLGL
 Sbjct: 11 ELSVGVGGGGGAAAPRAAEPAVQISLGRLILAGMVAGGVQYGVWALQLSLLTPVQTLGLS 70

Query: 83 -PIAGDRCTSFWMWC-----VGLYS-----PFIITGCMLIIGAAAHGPR 119
 + TSMWLC VGLYS PFIITGC+LI
 Sbjct: 71 HAL-----TSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFIITGCVLI----- 117

Query: 120 WLDFSMADLCFCSSNNWWETCCEAVFLVLVLPYRAEVETECVAVIVDTKE--L--G-- 172
 C AV ++V + A++ A + D+KE L G
 Sbjct: 118 -----CLAV--IIVGFSADIG---AALGDSKEECSLYHGPR 148

Query: 173 -HAAIVY-----NNTVQG-----D---HHGPSA-----LGNIL---- 196
 HAAIVY NNTVQG D HGPSA LGNIL
 Sbjct: 149 WHAAIVYVLGFWLDFSNNTVQGPARALMADLSAQHGPSAANSIFCSWMALGNILGYSSG 208

Query: 197 -----KWFVFVGFSHDHCSLYVLGFWPARAMA----ANSIGYSSGLKTS AFLVAV-- 242
 KWFVF+ R A AN LK AFLVAV
 Sbjct: 209 STNNWHKFPL-----RTRACCEACAN-----LK-GAFLVAVLFL 243

Query: 243 -----I FAKE-----ANLKGACLTVTLNENLPTTKAGG----PTGPLALAVLK-- 281
 I FAKE A LP TKA G PTGP LAV K
 Sbjct: 244 SLALVITLIFAKEVPYKAIA-----PLP-TKANGQVEVEPTGP--LAVFKGF 287

Query: 282 -----MPSVLLVT-----FPFILYDTDHGDPKLYSNAGFKDLPPAITWLSWWMGREI 328
 MPSVLLVT FPFILYDTD WMGREI
 Sbjct: 288 KNLPPGMPSVLLVTGLTWLSWFPFILYDTD-----WMGREI 323

Query: 329 Y-----QISAFNE-----LLLNSVIL-----PMCRKVGP-----FMV 355
 Y + +AF E LLLNSV+L PMC++GP +V
 Sbjct: 324 YHGDPKGTPAEANAFQEGVRAGAFGLLNSVVLGFSSFLIEPMCKRLGPRVVWVSSNMLV 383

Query: 356 CVAMASLRDYHGYSIKAVCSVGVRVGAFGGFSSFLIERVVWVTSNISFW----- 404
 C++MA A+C I IS+W
 Sbjct: 384 CLSMA-----AIC-----I-----ISWWATQDLHGYIQH 407

Query: 405 -ITAN-----AFLGVPTAQLAATALVQDAVLFA-PFAV-----GLCT 439
 ITA+ AFLG+P L A+L++ PFAV GLCT
 Sbjct: 408 AITASKEIKAVSLALFAFLGIP---L-----AILYSVPFAVTAQLAANKGGGQGLCT 456

Query: 440 GVLNIATRGGGQSIVIPQVIIAL-----NIPAF-----VVGFAVSA 476
 GVLNIA IVIPQVIIA+ NIPAF VVG+F
 Sbjct: 457 GVLNIA-----IVIPQVIIAVGAGPWDELFKGKNI PAFGMASVFA LIGGVVGIF--- 505

Query: 477 GGGVASALLPKIGHFALVGSKRQFR 501
 LLPKI S+RQFR
 Sbjct: 506 -----LLPKI-----SRRQFR 516

Score = 59.6 bits (133), Expect = 3e-07
 Identities = 39/107 (36%), Positives = 39/107 (36%), Gaps = 66/107 (61%)

Query: 1 MARGDGRG-----AA--AV-----RLILAG-----ALQLSL- 24
 MARG G G AA AV RLILAG ALQLSL
 Sbjct: 1 MARGGGNGEVELSVGVGGGGGAPRAAEPAVQISLGRLLAGMVAGGVQYGWALQLSLL 60

Query: 25 -----SHALTS-----VVQP---L-----RWGRRR 41
 SHALTS VVQP L RWGRRR
 Sbjct: 61 TPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTS RWGRRR 107

>gi|20152871|gb|AAM13408.1| sucrose transporter SUT1A [Triticum aestivum]
 Length = 522

Score = 303 bits (709), Expect = 8e-81
 Identities = 219/698 (31%), Positives = 244/698 (34%), Gaps = 435/698 (62%)

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQTL 79
 ELS GV VD ISLG MVAGGVQYGW LTPYVQTL
 Sbjct: 11 ELSVGVGAGAGGADAPAVD---ISLGRLLAGMVAGGVQYGWALQLSLLTPYVQTL 66

Query: 80 GLG-PIAGDRCTSFMWL-----VGLYS-----PFILTGCMLIIGAAH 116
 GL + TSFMWL VGLYS PFILTGC+LI
 Sbjct: 67 GLSHAL-----TSFMWLCGPIAGLVVQPCVGLYSDKCTS RWGRRRFILTGCILI---- 116

Query: 117 GPRWLDFSMADLCFCSSNNWWETCCEAVFLVLVPYRAEVETECVAVIVDTKE---L-- 171
 C AV V+V + A++ A + D+KE L
 Sbjct: 117 -----CIAV--VVVGFSADIG---AALGDSKEECSLYH 144

Query: 172 G---HAAIVYNNNTVQGDHHGPSALGNILKWFPVGFSSDHCSLYVLGFW----- 217
 G HAAIV YVLGFW
 Sbjct: 145 GPRWHAIAV-----YVLGFWLDFSNNTVQG 170

Query: 218 PARA-MA-----ANSI-----GYSSG-----LKT----- 235
 PARA MA ANSI GYSSG L+T

Sbjct: 171 PARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPLRTRACCEACAN 230
 Query: 236 --SAFLVAVIFAKEANLKG-A-CLTVTL--NEN-----LPTTKAGG----PTGPLAL 277
 AFLVAV+F L A CL +T+ E LPT KA G PTGPLA
 Sbjct: 231 LKGAFLVAVLF----L--AFCLVITVIFAKEIPIYKAIAPLPT-KANGQVEVEPTGPLA- 281
 Query: 278 AVLKMPSVLLVTFPFILYDTDHGDPKLYSNAGFKDLPPAI-----TWLSW----- 322
 V K GFK+LPP + TWLSW
 Sbjct: 282 -VFK-----GFKNLPPGMPSVLLVTGLTWLSWFPFILY 313
 Query: 323 ---WMGREIYQISAFNELLNSVILPMCRKVGPFMVCVAMASLRDYHG-----YSI 370
 WMGREI YHG +
 Sbjct: 314 DTDWMGREI-----YHGDPKGTPDEANAF 337
 Query: 371 KAVCSVGVRVGA-FG-----GFSSFLIE-----RVVWVTSN-----IS 402
 +A GVR GA-FG GFSSFLIE RVVWV+SN IS
 Sbjct: 338 QA---GVRAGAFGLLNSVVLGFSSFLIEPLCKRLGPRVVWVSSNFLVCLMSAAICIIS 393
 Query: 403 FW-----ITAN-----AFLGVPTAQLAATALVQDAVLFA-PFAV--- 435
 +W ITA+ AFLG+P L A+L++ PFAV
 Sbjct: 394 WWATQDLHGYIQHATASKEIKIVSLALFAFLGIP-----L---AILEYSVPFAVTAQ 442
 Query: 436 -----GLCTGVLNIA TRGGGQSIVIPQVIIAL-----NIPAFVVGVFAV 474
 GLCTGVLNIA IVIPQVIIA+ NIPAF
 Sbjct: 443 LAANRGGGQGLCTGVLNIA-----IVIPQVIIAVGAGPWDELFGKGNIPAF----- 488
 Query: 475 SAGGGVASA-----LLPKIGHFALVGSKRQFR 501
 GVASA LLPKI S+RQFR
 Sbjct: 489 ----GVASAFA-LIGGIVGIFLLPKI-----SRRQFR 515

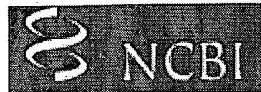
Score = 60.4 bits (135), Expect = 2e-07
 Identities = 38/106 (35%), Positives = 38/106 (35%), Gaps = 65/106 (61%)

Query: 1 MARGDGRG-----AAAV----RLILAG-----ALQLSL-- 24
 MARG G G A AV RLILAG ALQLSL
 Sbjct: 1 MARGGGNGEVELSVGVGAGAGGADAPAVDISLGRLILAGMVAGGVQYGWALQLSLLT 60
 Query: 25 -----SHALTS-----VVQP--L-----RWGRRR 41
 SHALTS VVQP L RWGRRR
 Sbjct: 61 PYVQTLGLSHALTSFMWLCLGPIAGLVVQPCVGLYSDKCTS RWGRRR 106

□>gi|19548165|gb|AAL90455.1| sucrose transporter SUT1D [Triticum aestivum]
 gi|20152875|gb|AAM13410.1| sucrose transporter SUT1D [Triticum aestivum]
 Length = 523

Score = 301 bits (703), Expect = 5e-80
 Identities = 217/699 (31%), Positives = 244/699 (34%), Gaps = 436/699 (62%)

Query: 46 ELSAGV-----VDHVAPISLG-----MVAGGVQYGW-----LTPYVQT 78
 ELS GV VD ISLG MVAGGVQYGW LTPYVQT
 Sbjct: 11 ELSVGVGGGGGAAAGGGEQPAVD---ISLGRLILAGMVAGGVQYGWALQLSLLTPYVQT 66
 Query: 79 LGLG-PIAGDRCTSFMWL-----VGLYS-----PFILTGCMLIIGAA 115
 LGL + TSFMWL VGLYS PFILTGC+LI
 Sbjct: 67 LGLSHAL---TSFMWLCLGPIAGLVVQPCVGLYSDKCTS RWGRRRFILTGCILI--- 117



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

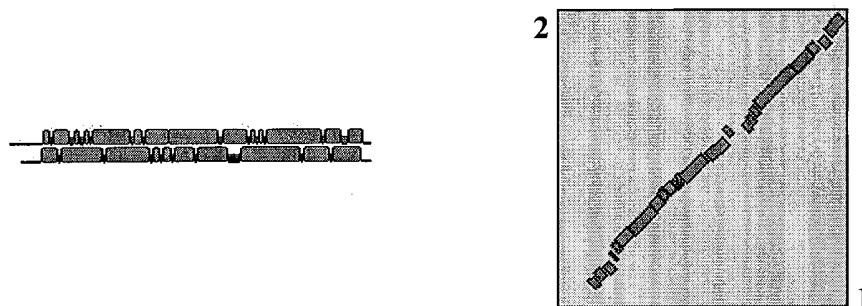
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.00000** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 501 (1 .. 501)

Sequence 2 lcl|seq_2 Length 510 (1 .. 510)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 42.0 bits (97), Expect = 0.066
 Identities = 115/512 (22%), Positives = 182/512 (35%), Gaps = 143/512 (27%)

Query: 62 VAGGVQYQGW-----LTPYVQTLGLGPIAGDRCTSFMWLC-----VGLYS--- 100 SEQ ID NO: 2
 +A GVQ+GW LTPYVQ LG+ + +++WLC VG YS

Subjct: 40 IAAGVQFGWALQLSLLTPYVQLLGI-----HKWAAYIWLCGPISGMLVQPIVGYYSDRCQ 95 GI4091871

Query: 101 -----PFIITG--CMLIIGAAHGPRWLLDFSMADLCFCSSNNWEETCCEAVFLVLV 151
 PFI +G C+ I G + + D + T T F +L

Subjct: 96 SSFGRRRPFIASGAGCVAISVILIGFAADIGYKAGD--DMNKTLPRAVTVFVIGFWILD 153

Query: 152 PYRAEVETECVAVIVD-----TKELGHAAIVYN-----NTVQGDHHGPSALGNILKWFPF 201
 ++ C A++ D T+ + A +Y + G+ G + N+ K FPF

Subjct: 154 VANNMLQGPCRALLADLCNGDTRRMRSANALYRFFMAVGNILGNAAG--SYNNLYKLFPP 211

Query: 202 VGFSSDH-CSLYVLGFWRARAMAANSIGYSSGLKTS AFLVAVIFAKEANLKGACLTVTLN 260
 S H C LY A + I + + + V+ K+ + A +

Subjct: 212 ---SKTHACDLYC----ANLKSCFIISIVLLIFITVLALT VVREKQWSPDEA-----D 257

Query: 261 ENLPTTKAGGPTGPLALAVLKMPSVLLVT-----FPFILYDTDHGDPKLYSNAG 309
 E P++ G L A+ +P +L+ FPFIL+DTD

Subjct: 258 EEPSSSGKIPVFGELLRALKDLPRLPMLLLAVTCLNWIAWFPPFILFDTD----- 306

Query: 310 FKDLPPAITWLSWWMGREIY----QISAFNE-----LLLNSV-----ILPMCRK 349
 WMGREIY Q +++ LLLNSV + + R

Subjct: 307 -----WMGREIYGGTAGQGKLYDQGVRVGSLGLLNSVGLTSIAVEYLVRG 353

Query: 350 VGP FMVCVAMASLRDYHGYSIKAVCSVGVRVGAFGGFSSFLIERVVWVTSNISFWITANA 409
 VG + + + G + V S + G + L+ + S + +

Sbjct: 354 VGGVKILWGLVNFLLAIGLVMTVVSKVAQHQRQHGANGQLLPPSAVKAGALSLF----S 409

Query: 410 FLGVPTAQLAATALVQDAVLFAPFAV--GLCTGVLNIA TRGGGQSIVIPQVIAL---- 462
LG+P + + ++ + GL GVLN+A IV+PQ+I+++

Sbjct: 410 ILGIPLSITFSIPFALASIYSSSGGAGQGLSLGVLNLA-----IVVPQMTIVSVLAGPF 462

Query: 463 -----NIPXXXXXXXXXXXXXXXXXXLPK 487

N+P LLPK

Sbjct: 463 DSLFGGGNLPAFVVGAISAAISGVLAIVLLPK 494

CPU time: 0.35 user secs. 0.05 sys. secs 0.40 total secs.

| Lambda | K | H |
|--------|-------|-------|
| 0.325 | 0.140 | 0.450 |

Gapped

| Lambda | K | H |
|--------|--------|-------|
| 0.267 | 0.0410 | 0.140 |

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 2284

Number of Sequences: 0

Number of extensions: 222

Number of successful extensions: 5

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 1

Number of HSP's that attempted gapping in prelim test: 1

Number of HSP's gapped (non-prelim): 1

length of query: 501

length of database: 776,568,843

effective HSP length: 135

effective length of query: 366

effective length of database: 776,568,708

effective search space: 284224147128

effective search space used: 284224147128

T: 9

A: 40

X1: 15 (7.0 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 40 (21.6 bits)

S2: 79 (35.0 bits)